



SEQUENCE LISTING

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NOV 01 2002

· 112 ·

RECEIVED

· 113 ·

· 14 · US 09/661,992

· 15 · 106

· 16 · PatentIn Ver. 2.1

· 210 · 1

· 211 · 16

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of the artificial sequence:primer

· 400 · 1

atggattttc ttgtccacct tgggtgc

26

· 210 · 1

· 211 · 16

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of the artificial sequence:primer

· 400 · 2

ttcgattttc ttgtatcaact cagtct

26

· 210 · 3

· 211 · 34

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of the artificial sequence:primer

· 400 · 3

ttggatatgggc acatgcagat ctct

24

· 210 · 4

· 211 · 34

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

· 223 · Description of the artificial sequence:primer

· 400 · 4

tttcatttcgt ttgaagctct tgac

24

• 210: 5
• 211: 10
• 212: FPT
• 213: Artificial Sequence

• 220:
• 223: Description of the artificial sequence: CDR3 region

• 400: 5
Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr
1 5 10

• 211: 6
• 212: 12
• 213: FPT
• 214: Artificial Sequence

• 220:
• 223: Description of the artificial sequence: CDR3 region

• 210: 6
Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr
1 5 10

• 211: 7
• 212: 13
• 213: FPT
• 214: Artificial Sequence

• 220:
• 223: Description of the artificial sequence: CDR3 region

• 400: 7
Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

• 210: 8
• 211: 13
• 212: FPT
• 213: Artificial Sequence

• 220:
• 223: Description of the artificial sequence: CDR3 region

• 400: 8
Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

• 210: 9
• 211: 14
• 212: FPT
• 213: Artificial Sequence

• 220:
• 223: Description of the artificial sequence: CDR3 region

• 400: 9

Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

· 110 · 10
· 111 · 13
· 112 · PFT
· 113 · Artificial Sequence

· 120 ·
· 123 · Description of the artificial sequence:CDR3 region

· 400 · 10
Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr
1 5 10

· 110 · 11
· 111 · 16
· 112 · PFT
· 113 · Artificial Sequence

· 120 ·
· 123 · Description of the artificial sequence:CDR3 region

· 400 · 13
Glu Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

· 210 · 12
· 211 · 18
· 212 · PFT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence:CDR3 region

· 400 · 13
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

· 210 · 13
· 211 · 18
· 212 · PFT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence:CDR3 region

· 400 · 13
Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu
1 5 10 15

Trp Glu

· 210 · 14
· 211 · 15
· 212 · PRT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence: CDR3 region

· 400 · 14
Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly
1 5 10 15

Asp Glu

· 210 · 15
· 211 · 16
· 212 · PRT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence: CDR3 region

· 400 · 15
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

· 210 · 16
· 211 · 18
· 212 · PRT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence: CDR3 region

· 400 · 16
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

· 210 · 17
· 211 · 18
· 212 · PRT
· 213 · Artificial Sequence

· 220 ·
· 223 · Description of the artificial sequence: CDR3 region

· 400 · 17
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 18
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 18
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 19
Arg Arg Arg Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 20
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 20
Arg Arg Arg Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 21
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 21
Arg Arg Arg Glu Gly Ala Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

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-210: 22
-211: 16
-212: PFT
-213: Artificial Sequence

-220:
-223: Description of the artificial sequence:CDR3 region

-230: 21
Arg Arg Arg Glu Gly Gly Ala Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

-210: 23
-211: 16
-212: PFT
-213: Artificial Sequence

-220:
-223: Description of the artificial sequence:CDR3 region

-230: 23
Arg Arg Arg Glu Gly Gly Ala Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

-210: 24
-211: 16
-212: PFT
-213: Artificial Sequence

-220:
-223: Description of the artificial sequence:CDR3 region

-230: 24
Arg Arg Arg Glu Gly Gly Tyr Ala Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

-210: 25
-211: 16
-212: PFT
-213: Artificial Sequence

-220:
-223: Description of the artificial sequence:CDR3 region

-230: 25
Arg Arg Arg Glu Gly Gly Tyr Tyr Ala Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

W210: 26
W211: 18
W212: PPT
W213: Artificial Sequence

W210:
W213: Description of the artificial sequence:CDR3 region

W400: 26
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Ala Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

W210: 17
W211: 18
W212: PPT
W213: Artificial Sequence

W210:
W213: Description of the artificial sequence:CDR3 region

W400: 17
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Ala Tyr Phe Asp Arg
1 5 10 15

Arg Arg

W210: 18
W211: 18
W212: PPT
W213: Artificial Sequence

W210:
W213: Description of the artificial sequence:CDR3 region

W400: 18
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Ala Phe Asp Arg
1 5 10 15

Arg Arg

W210: 19
W211: 18
W212: PPT
W213: Artificial Sequence

W210:
W213: Description of the artificial sequence:CDR3 region

W400: 19
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1

5

10

15

Arg Arg

<210> 30

<211> 16

<212> PRT

<213> Artificial Sequence

<400>

<423> Description of the artificial sequence:CDR3 region

<400> 31

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg
1 5 10 15

Arg Arg

<210> 31

<211> 16

<212> PRT

<213> Artificial Sequence

<211>

<423> Description of the artificial sequence:CDR3 region

<400> 31

Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg
1 5 10 15

Arg Arg

<210> 32

<211> 18

<212> PRT

<213> Artificial Sequence

<400>

<423> Description of the artificial sequence:CDR3 region

<400> 32

Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 33

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<423> Description of the artificial sequence:CDR3 region

<400> 33

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 34

<211> 18

<212> PRT

<213> Artificial Sequence

<410>

<413> Description of the artificial sequence:CDR3 region

<400> 34

Arg Arg Arg Glu Gly Gly Glu Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 35

<211> 18

<212> PRT

<213> Artificial Sequence

<410>

<413> Description of the artificial sequence:CDR3 region

<400> 35

Arg Arg Arg Glu Gly Gly Glu Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 36

<211> 18

<212> PRT

<213> Artificial Sequence

<410>

<413> Description of the artificial sequence:CDR3 region

<400> 36

Arg Arg Arg Glu Gly Gly Glu Tyr Glu Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 37

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<40> 37

Arg Arg Arg Glu Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<21> 38

<21> 18

<21> PRT

<21> Artificial Sequence

<22>

<22> Description of the artificial sequence:CDR3 region

<40> 38

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<21> 39

<21> 18

<21> PRT

<21> Artificial Sequence

<22>

<22> Description of the artificial sequence:CDR3 region

<40> 39

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Glu Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<21> 40

<21> 18

<21> PRT

<21> Artificial Sequence

<22>

<22> Description of the artificial sequence:CDR3 region

<40> 40

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Glu Phe Asp Arg
1 5 10 15

Arg Arg

<21> 41

<21> 18

<21> PRT

<21> Artificial Sequence

<22>

<22> Description of the artificial sequence:CDR3 region

<400> 41

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Glu Asp Arg
1 5 10 15

Arg Arg

<210> 42

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 42

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg
1 5 10 15

Arg Arg

<210> 43

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 43

Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 44

<211> 18

<212> PPT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 44

Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 45

<211> 14

<212> PPT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 45

Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10

4210: 46

4211: 14

4212: PRT

4213: Artificial Sequence

4220:

4223: Description of the artificial sequence:CDR3 region

4400: 46

Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp
5 10

4410: 47

4411: 18

4412: PRT

4413: Artificial Sequence

4420:

4423: Description of the artificial sequence:CDR3 region

4430: 47

Glu Glu Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu
5 10 15

Glu Glu

4510: 48

4511: 18

4512: PFT

4513: Artificial Sequence

4520:

4523: Description of the artificial sequence:CDR3 region

4440: 48

Arg Arg Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

4610: 49

4611: 18

4612: PFT

4613: Artificial Sequence

4620:

4623: Description of the artificial sequence:CDR3 region

4400: 49

Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg
1 5 10 15

Arg Arg

<210> 50
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 50
gtatcgatga ctgcggccca agccggccat gcccsaggtt marctgcags agtcwgg 57

<210> 51
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 51
gtatcgaa ctgcggccca gccggccatg gccgaggtgc agttcagga gtcagg 56

<210> 52
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 52
gtatcgaa ctgcggccca gccggccatg gccgatgtgc agttcagga gtcagg 56

<210> 53
<211> 56
<212> RNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 53
gtatcgaa ctgcggccca gccggccatg gcccaggtgc agctgaagsa gtcagg 56

<210> 54
<211> 56
<212> RNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 54
gtatcgaa ctgcggccca gccggccatg gccgaggttc agctgcarca rtctgg 56

<210> 55
<211>

<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<4> 5:
atccatcgaaa ctggggccca gcccggccatg gcccagggttc arctgcagca gycgtgg 56

<210> 5:
<211> 5:
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<4> 5:
atccatcgaaa ctggggccca gcccggccatg gcccagggttc agctgggttga rtctgg 56

<210> 5:
<211> 5:
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<4> 5:
gtccatcgaaa ctggggccca gcccggccatg gcccagggttc agcttcagca gtctgg 56

<210> 5:
<211> 5:
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<4> 5:
gtccatcgaaa ctggggccca gcccggccatg gcccagggttc agctgktgg 56

<210> 5:
<211> 5:
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<4> 5:
gtccatcgaaa ctggggccca gcccggccatg gcccaggatcc agttgctgca gtctgg 56

<210> 6:
<211> 6:
<212> DNA
<213> Artificial Sequence

... Description of the artificial sequence:primer
-411- 61
-412- cgcgcgcac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc 60
-413- 61
-414- 6
-415- DNA
-416- Artificial Sequence
-417-
-418- Description of the artificial sequence:primer
-419- 61
-420- cgcgcgcac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc 60
-421- 61
-422- 6
-423- DNA
-424- Artificial Sequence
-425-
-426- Description of the artificial sequence:primer
-427- 61
-428- cgcgcgcac ctgaaccgcc tccacctgca gagacagtga ccagagtccc 60
-429- 64
-430- 60
-431- DNA
-432- Artificial Sequence
-433-
-434- Description of the artificial sequence:primer
-435- 64
-436- cgcgcgcac ctgaaccgcc tccacctgag gagacggtga ctgaggttcc 60
-437- 65
-438- 60
-439- DNA
-440- Artificial Sequence
-441-

ggttcagatg ggcgcgcctc tggcggtggc ggatcgsaaa wtgtkctcac ccagtctcc 59

<210> 71
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<40> 71
gtttcagatg ggcgcgcctc tggcggtggc ggatcggaya tyvwgatgac mcagwctcc 59

<210> 72
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<40> 72
gtttcagatg ggcgcgcctc tggcggtggc ggatcgaaa ttgttctcac ccagtctcc 59

<210> 73
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<40> 73
gtttcagatg ggcgcgcctc tggcggtggc ggatcgcat tattcaggt gcttgtgg 59

<210> 74
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<40> 74
gtatcattct gggggggccc gtttgatttc cagcttggtg cc 42

<210> 75
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<40> 75
jagtcatctt gggggggccc gttttatttc cagcttggcc cc 42

<210> 76
<211> 42
<212> DNA
<213> Artificial Sequence

<214>
<215> Description of the artificial sequence:primer

<401> 76
:49: tattctt gggggggccc gtttttatttc cagtctggtc cc 42

<211> 77
<212> 42
<213> DNA
<214> Artificial Sequence

<215>
<216> Description of the artificial sequence:primer

<401> 77
:50: tattctt gggggggccc gtttttatttc caactttgtc cc 42

<211> 78
<212> 42
<213> DNA
<214> Artificial Sequence

<215>
<216> Description of the artificial sequence:primer

<401> 78
:51: tattctt gggggggccc gtttcagctc cagttggtc cc 42

<210> 79
<211> 74
<212> DNA
<213> Artificial Sequence

<214>
<215> Description of the artificial sequence:mychis 6

<401> 79
:52: gggggggaaa caaaaactca tctcagaaga ggatctgaat gggggggcac atcaccatca 60
ttatcactaa taag 74

<210> 80
<211> 74
<212> DNA
<213> Artificial Sequence

<214>
<215> Description of the artificial sequence:mycchis

<401> 80
:53: ttatttattt agtgatggtg atggtgatgt gccggcccat tcagatcctc ttctgagatg 60
tgtttttgtt ctgc 74

<216> 81

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 81

ggggaaagg tggggaggc tggacctgag ctgaagaagg ctggagagac agtcaagatc 60
tttttcaagg cttttggta tattttccaa aactatggaa tgaactgggt gaagcaggct 120
ttggaaaagg gttttaaagtg gatgggctgg ataaacacct acactggaga gccaacatat 180
ttttgtgtact tcaaggacg gtttgccttc tttttggaaa cttttgcacg cactgcctat 240
tttttgtatca acaaccccaa aaatgaggac acggctacat atttttgtgc atttatatgg 300
ttttcccta aggggtttgc ttactggggc caaggaaatc tggttcactgt ctttgcagg 360
gggggggtt cagggtggcg cggctctggc ggtggggat cggatattca gatgacacag 420
ttttttcaat ttctgttgtt atcagcaggaa gacagggttta cttttttttt caaggccagt 480
tagatgttga gtaatgtatgt agtttggtaa caacagaagg cggggcagtc ttctaaacta 540
ttgtatgtact atgtatccaa ttgttacact ggagtccctg atcgtttca c tggcagtgg 600
ttatgggggg attttcaatcc cccatccaa actgttccagg ctgaaggaccc ggcactttat 660
ttttttttttt aggtttatgg ctttttttcc acgttccggat gggggccaccaa gctggaaatt 720
aaaaacgg 726

<410> 82

<411> 342

<412> PRT

<413> Artificial Sequence

<420>

<423> Description of the artificial sequence:scFv region

<440> 82

Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Lys Gin Ala Pro Gly Lys Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe
130 135 140

Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln

472

— 8 —

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Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val
 160 165 170 175

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
195 200 205

Le Ser Thr Val Gln Ala Glu Asp Ieu Ala Val Tyr Phe Cys Gln Gln
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 125 230 235 240

Lys Arg

1120 83

. 11: 747

112) DNA

• (13) Artificial Sequence

120

• 123: Description of the artificial sequence: scFv region

1223-32

- 220 - 14

- 11 - 243

• 100 • FRT

• 13 • Artificial Sequence

22, 11.

3.1.3. Description of the artificial sequence: scFv region

420 84

Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

Ter Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Ile Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 65 70 75 80

Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
 100 105 110 115

Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 115 120 125

Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro
 130 135 140

Leu Ser Leu Pro Val Ser Ile Gly Asp Gln Ala Ser Ile Ser Cys Arg
 145 150 155 160

Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp
 165 170 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 180 185 190

Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 210 215 220

Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly
 225 230 235 240

Gly Gly Thr Lys Leu Gln Ile Lys Arg
 245

• 110 - 65
• 111 - 747
• 112 - DNA
• 113 - Artificial Sequence

1410 - 65
 gggtgtgcaga ttcaaggagtc aggggggagtc ttatgtcaagg ctggagggtc cctgaaaactc 60
 tccttctycaag cctctggatt caattttcaatg agctataccca tgctctgggt tccgcagact 120
 ccggagaagaaga gggtggagtg ggtcgcaacc attagtagtg gtggtagtgc caactactat 180
 ccggccatgtg tgaaggggccj attcaccatc tccagagaca atgcacaagaa caacctgtac 240
 ctgcataatgtc gcagtctcgag gtctgaggac acaggccatgt attactgtac aagagaggggg 300
 gatgttttca cccgtcaacty gtactttagat gtctggggccj cagggactct ggtcaactgtc 360
 ttatgcagggtg gaggcggttc aggtggggcgc gcttctggcg gtgggggatc gggaaaatgtg 420
 ctcaaccatgt ctccatgttc ttctggctgtc tctcttagggc agagggggccac cttatctctgc 480
 aaacccatgtg aaagtgttgc tagtttatggc tataatttttca tggactggta tcagcagata 540
 tttggccacgc caaccaaaact cttccatctat cgtgcacatca accttagagtc tgggatccct 600
 ttccatgttca gtggccatgttgg ctcttaggaca gacttccatcc tccaccattaa ttctgtggag 660
 ctgtgtatgttgc ttgcacacttca ttactgtcaag caaagtaatg aggtatccgtc caccgttcgg 720
 ctgtgtatgttgc ttgcacacttca ttactgtcaag caaagtaatg aggtatccgtc caccgttcgg 747

4210. 36
4211. 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 86

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Ile Val Lys Pro Gly Gly
1 5 10 15

Ser Ile Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30 35

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Thr Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Ser Gly
115 120 125

Gly Arg Ala Ser Gly Gly Ser Gly Ser Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 87

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

Figure 1. A schematic diagram of the model.

1110 • JGIM

111 249

112 PRT

• 130 • Artificial Sequence

202

1.23) Description of the artificial sequence: scFv region

• 400 • 83

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Ieu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
85 90 95

Tar Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110

Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Arg Ala Ser Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
 130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
 165 170 175

Tyr Gin Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 185 186 187 188

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser

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200

11

Arg Thr Asp Phe Thr Ile Thr Ile Asn Pro Val Glu Ala Asp Asp Val
310 315 320

Ala Thr Tyr Tyr Cys Gin Gin Ser Asn Glu Asp Pro Leu Thr Phe Gly
2.6 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244

Ala Ile Thr Arg Leu Glu Ile Lys Arg
245

4.10 - 69

4.11.2199

4.12 · DNA

4.13. Artificial Sequence

211

4.2.3. Description of the artificial sequence: scFv region

• 49(1), 199

atggaaatacc tattggctac ggcagcggtt ggattttat taatcgccgc ccayccggcc 60
atggcgaaagg tgaaggcttgtt ggaytcgtgg ggaggcttag tgaaggctgg aggytcgttg 120
aaactctct gtgcagccctt tggattract ttcaatgttcc ataccatgttcc ttgggttcc 180
.aaactccgg aaaaagggtt gggatgggtt gaaacatattt gtaatgggttcc ttggatcc 240
taatatccgg acatgtgaa gggccgttcc acaatctccaa gagaaatgttcc caaaatcc 300
ttgttacatgc aaaaatggcag ttgtgggttcc gggggccatgg tttatgttcc ttgttacatgc 360
gggggggttcc gtttccatgttcc aactgttcc ttggatgttcc ttggccgttcc aactgttcc 420
acgttccatgttcc aagggtgggg tgggttccatgttcc ttggatgttcc ttggatgttcc 480
ttgttccatgttcc acaatgttcc agtttccatgttcc ttgttccatgttcc ttggatgttcc 540
ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 600
aaatccatgg gacagccatcc aaaaacttcc atccatgttcc ttgttccatgttcc aatccatgg 660
ttttatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 720
ttggatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 780
ttccggatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 840
ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 900
ttaaatccatgg atccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 960
ttttatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1020
cccgaaagggttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1080
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1140
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1200
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1260
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1320
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1380
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1440
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1500
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1560
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1620
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1680
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1740
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1800
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1860
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1920
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 1980
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 2040
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 2100
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 2160
ttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc ttgttccatgttcc 2220

12100-97

43110-732

(212) PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: scFv region

<400> 90

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gin Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp
145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gin
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala
275 280 285

Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp
290 295 300

Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn
305 310 315 320

Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala
325 330 335

Ala Arg Asn Tyr Ala Glu Gly Ala Gly Phe Phe Lys Gly Ile Asp
340 345 350

Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys
355 360 365

Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala
370 375 380

Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile
385 390 395 400

His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly
405 410 415

Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro
420 425 430

Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser
435 440 445

Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Lys
450 455 460

Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu
465 470 475 480

Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp
485 490 495

Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu
500 505 510

Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln
515 520 525

Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp
530 535 540

Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val
545 550 555 560

Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala
565 570 575

Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly
580 585 590

Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala
595 600 605

Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala
610 615 620

Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val
625 630 635 640

Ile Val Thr Ala Asp His Ala Asp Ala Ser Gln Ile Val Ala Pro Asp
645 650 655 660 665

Thr Lys Ala Pro Gly Ileu Thr Gln Ala Ileu Asn Thr Lys Asp Gly Ala
660 665 670

Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Glu Glu His
678 686 694 696 698 700 702 704 706 708 710 712 714 716 718 720

Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn
690 695 700

Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala
 735 740 745 750 755 760 765 770

Ala Leu Gly Asp Ile Ala His His His His His His His
725 730

Q110: 91
Q111: 978
Q112: DNA
Q113: Artificial Sequence

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723) Description of the artificial sequence: scFv region

400 G1

atgaaataacc tattgcctac ggcagccgt ggattgttat tactcgccgs ccagccggcc 60
 atgggggagg tgaaggttgt ggagtctggg ggagggtttag tgaagctgg agggtsctg 1.0
 aaaccttctt gtgcagcctc tggattcaet ttcaagtagst ataccatgtt ttgggttcgs 140
 tggaaatccgg agaaaggaggtt ggagtgggtc gcaacccatta gtatggnnng tagttccacc 243
 tactatccag acagtgtgaa gggccgattc accatctccg gagacaatgtc caagaacacc 310
 ctgtacccgtc aaatggacag tctgaggtct gaggacacag ccattgttattt ctgtacaaga 360
 ggggggggtt gtttccacgtt caacttgttac ttccatgttcc gggggccggg aacctcaatg 420
 accgttcttcg cagggtggagg cgggttcajgtt gggggccgtt ctggccgggtgg cggatccggac 480
 atttgtgttca cacaatntcc agcttcttccg tctgtgttccg tagggccagat ggcacaccata 540
 tttttccatgg ccaatgttccaaag tttttgtatgtt tttttgttccatgg tttttatgttcc 600
 cccatccatgg gacacccccc cccatccatgg tttttatgttccatgg tttttatgttcc 660
 atccatccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 720
 atccatccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 780
 tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 840
 tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 900
 tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 960
 tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttccatgg tttttatgttcc 978

421 0 92
42111 315
42100 PRT
42130 Art

1.1.1. Functional Sequences

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2.2.1. Description of the artificial sequence: scFv region

4 JU. 92

Met Lys Tyr Ileu Leu Pro Thr Ala Ala Ala Gly Leu Ileu Leu Leu Ala
1 5 10 15

Aia Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 20 25 30

Le1 Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

35	40	45
Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu		
50	55	60
Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr		
65	70	75
Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn		
85	90	95
Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Ile Arg Ser Glu Asp		
100	105	110
Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn		
115	120	125
Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser		
130	135	140
Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp		
145	150	155
Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln		
165	170	175
Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly		
180	185	190
Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys		
195	200	205
Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg		
210	215	220
Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro		
225	230	235
Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu		
245	250	255
Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala		
260	265	270
Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln		
275	280	285
Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu		
290	295	300
Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His		
305	310	315
His His His His His		
325		

<210> 93
 <211> 2190
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

卷之三

atgatatacc tattgtccatc ggccaggccgtt ggatgtttat taatccggggc ccaggccggcc 61
 atggccgagg ttcaagttca gcaagtatggc ttctggatgggg tgaagccccc ggcctcagtg 126
 aagatttccot gcaaaagcttc tggatcagca ttcaagttatc ttgtggatggaa ctgggttgaag 186
 cagaigctg gacagggtct tggatggatt ggacggattt atccctggaaa tggagatact 249
 aacttcaatg ggaagttcaa ggccaaaggcc acactgatctg cagacaaaatc ttccaaacaca 301
 gcttccatgc agctcagcag ttctggatctt ttggactctg cggctctattt ttgttgagat 360
 ggttaacccat attactatgc ttatggactac tggggtccaa gaaacctcagt caccgtctcc 420
 tcagttggag gggttccagg tggccggcc ttctgggggtg gcggatcgc aatttgttctc 460
 accccgttcc ttgttttctt tggatgtatct ttggggcaga gggccacccat ttcatgcagg 540
 gccaacaaaa ttgttcaagttac ttctggatctt agttatatgc actggatccaa acagaaacca 600
 ggacagccaa cccaaacttcc ttatctatctt gcatccaaacc taaaatgtgg ggtccctggc 660
 aggttcaatg gcaatgggtt tggggacagac ttcaacccatc acatccatcc ttgtggaggag 720
 gaggatgtctt caaaatattttt ttgttccggcc acgttggggcc agttagggagc ttcttggac ttgtcggttgg 780
 gggccaaagg tggaaaatca gggggggcc gcaagccccc caccatggaaat gctgttttgg 840
 gaaaauccggc ttgttccgggg tggatattact gcaacccgggg ttgtctggcgg tttaaagggtt 900
 gatccatgtt ccgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc 960
 ctgttttggcc atgggtatggg ggacttggaa ttatctggcc cacgttaatc ttgtccaaagg 1010
 gggtttccgtt tttttaaagg ttatgtatcc ttacccgttta ccggggaaata cacttactat 1060
 gggtttcaata aaaaaacccgg cccaaacggcc taaatccggcc acgttccggcc atccgttcc 1140
 gtgttgttcc ccgttccgttcc ttatctatcc gggccgggtgg ggttccgtat ttccggaaatcc 1210
 gtatccccc ccatttttggc ttatggaaa gggccggggcc tggccggccgg taatcttttt 1260
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 ttgttccggcc ccggccggcc ccgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc 1370
 aaaggatgttcc ttacccggcc ttatctatcc ttgttccggcc acgttccggcc ttgttccggcc 1440
 gcaaaaaccc ttgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc 1510
 cggccggccgg ccgttccggcc ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 1580
 ggatggatcc acgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc ttgttccggcc 1650
 tggccggccgg ccggccggcc ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 1720
 cccaaatccggc aacatgtatcc ttgttccggcc acgttccggcc ttgttccggcc ttgttccggcc 1790
 ttatgttccgtt ttatggatcc ttatggatcc ttgttccggcc ttgttccggcc ttgttccggcc 1860
 aaacccggatcc ttgttccggcc ttatctatcc ttgttccggcc acgttccggcc ttgttccggcc 1920
 gggttccaaac gggccggccgtt ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 1980
 ttgttccggcc ccgttccggcc ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 2040
 ttatccggccgg ccgttccggcc ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 2100
 ttatgttccgtt gacttccggcc ccgttccggcc ttatctatcc ttgttccggcc ttgttccggcc 2160
 ttatccggccgg ccgttccggcc ttatctatcc ttgttccggcc ttgttccggcc ttgttccggcc 2190

221 3 94

4211 · 729

4212 PRT

4213 · Artificial Sequence

-22-

4.223 · Description of the artificial sequence: scFv region

1400 > 94

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala

On the other hand, the *ct* gene is expressed in the same way in all the tissues examined, with the exception of the testis, where it is expressed at a lower level.

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
100 105 110
Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
130 135 140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
145 150 155 160
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
165 170 175
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
180 185 190
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
195 200 205
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
210 215 220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
225 230 235 240
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
245 250 255
Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala
260 265 270
Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp
275 280 285
Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala
290 295 300
Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu
305 310 315 320
Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn
325 330 335
Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro
340 345 350
Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys
355 360 365
Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr
370 375 380
Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys
385 390 395 400

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr
405 410 415

Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu
420 425 430

Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser
435 440 445

Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile
450 455 460

Thr Glu Gln Leu Ile Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly
465 470 475 480

Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys
485 490 495

Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp
500 505 510

Ala Ala Ser Leu Asn Ser Val Thr Gln Ala Asn Gln Gln Lys Pro Ile
515 520 525

Ile Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro
530 535 540

Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr
545 550 555 560

Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr
565 570 575

Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu
580 585 590

Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro
595 600 605

Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg
610 615 620

Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr
625 630 635 640

Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala
645 650 655

Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val
660 665 670

Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Gln His Thr Gly Ser
675 680 685

Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly
690 695 700

Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly
705 710 715 720

Asp Ile Ala His His His His His His
725

... sequence

卷之三

4.2.3 Description of the artificial sequence: scFv region

2400 100

atgtatatacc	tattgtctac	gggttgtccgt	ggatgtttat	tactcgcggc	ccagccggcc	60
ttgggggagg	ttcagtttca	ccatgttgg	cctgagatgg	tgaagccccc	ggcttcagt	120
ggattttctt	gtaaaagctt	tggatcacca	ttcagtagct	tttggatgaa	cttgggttaag	180
tatcaatccct	gacagggtt	cgatgttgg	ggacccattt	atccatggaaa	tggagatact	240
aaacttcaat	ggaaagttaaa	ggggaaaggcc	acactgactg	ccacacaaatc	ctccagcaca	300
cccttcatgc	atctcagcag	cctgtacctt	gtggactctg	ccgttctattt	ctgtgcagat	360
ttgtatcgat	attactatgc	tatggactac	tgggttcaag	aaacccctagt	ccacgttctcc	420
tcaagtggag	ccggtttcagg	tggggcgcc	tctgggggtg	ccggatcgca	aattgttctc	480
ccccgttctc	ctgttttctt	agctgtatct	ctggggcaga	ggggccacccat	ctcatgcagg	540
gtgtatcaaaa	gtgtcagttac	atctggctat	agttatatgc	actggtacca	acagaaaaacca	600
ggacccgcac	ccaaactctt	catctatctt	gcatccaaacc	tagaatstgg	ggtcctgtcc	660
atgttcaatgt	gtggatgggtc	tggggacagac	ttccacccctca	acatccatcc	tgtggaggag	720
ttgggttgtct	caacccatttt	ctgtccaccc	agtaaggagg	ttccctggac	tttcgggtgg	780
gtgtatcaagg	tggaaaatcaa	acggggccgc	gcacccaaac	tttccactcc	ggccggggct	840
ttccatgtat	aaacgttgg	agacaaatgt	gaggagctc	ttaccaagaa	ctaccatcta	900
gtttatcgagg	tagtcgtct	aaaaaaatgtt	tttttttttttt	tttttttttttt	tttttttttttt	960
ccccatttaa						969

360

4.110 - 96
4.111 - 322
4.112 - PRT
4.113 - Artificial Sequence

• 120 •

4.223. Description of the artificial sequence: scFv region

(400) 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Glu Pro Ala Met Ala Glu Val Gin Leu Gln Gln Ser Gly Pro Glu
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Ala Phe Ser Ser Ser Itp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60

Gln Ile Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Tyr Ala Met
115 120 125

Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Ser-Val-Thr-Gln-Ser-Ser-Gly-Gly-Gly

130	135	140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu		
145	150	155
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr		
160	170	175
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr		
180	185	190
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile		
195	200	205
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly		
210	215	220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu		
225	230	235
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg		
245	250	255
Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro		
260	265	270
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp		
275	280	285
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val		
290	295	300
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His		
305	310	315
320		
His His		

4110: P7

4111: P70

4112: DNA

4113: Artificial Sequence

4120:

4121: Description of the artificial sequence:scFv region

4400: P7

caugguaaacag statgaccat gattacgcga agsttccatg aaaattctat ttcaaggaga 60
 caugtataat gaaataccta ttgcctacgg cagccgcgtgg attgttattta ctgcgcggccc 120
 aacccggccat ggcccgagggtg cagctgcagg cgccgcgtgca ggtcgaacctc gagatcaaac 180
 yggcggcgcgca agaacaaaaaa ctcatctcag aagaggatct gaatggggcg gcacatcacc 240
 ttcaaccatca ctaataagaa ttcaactggcc 270

4410: P8

4411: P1

4412: PRT

4413: Artificial Sequence

4420:

4421: Description of the artificial sequence:scFv region

<400> 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Ieu Ieu Ieu Ieu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Ieu Gln Ala Arg Ieu Gln Val
20 25 30

Asp Ieu Gln Ile Lys Arg Ala Ala Ala Gln Lys Ieu Ile Ser Gln
35 40 45

Alu Asp Leu Asn Gly Ala Ala His His His His His His
50 55 60

<411> 99

<411> 888

<411> DNA

<411> Artificial Sequence

<420>

<420> Description of the artificial sequence:scFv region

<400> 99

atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 60
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 120
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 180
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 240
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 300
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 360
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 420
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 480
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 540
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 600
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 660
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 720
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 780
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 840
atgtttatcc tattgtctac ggcagccgct ggattgttat tactcgccggcc 888

<411> 100

<411> 294

<411> PRT

<411> Artificial Sequence

<420>

<420> Description of the artificial sequence:scFv region

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Ieu Ieu Ieu Ieu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Ieu Val Glu Ser Gly Gly
20 25 30

Ieu Val Lys Pro Gly Gly Ser Leu Lys Ieu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Chr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

01100 101
01110 376
01120 DNA
01130 Artificial Sequence

4.1.6. Description of the artificial sequence: scFv region

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<400> 101
atgaaaatacc tattgcctac ggcagecggtt ggattgttat tactggggc ccagccggcc 60
atggccgagg ttcaagttca gcaagtcttgg aactgagctgg tggaaacccgg ggcctcaatgt 120
atgatttctt gcaaaatgttc tggctacqca tttagtagct ctggatgaa ctgggtgaag 180
cagaggcctg gacagggtct tgatgtggatt ggacgggattt atcttggaaa tggagatact 240
aaactacaatgt ggaagtttcaaa gggcaaggcc aactgtactgt cagacaaaatc ctccagcaca 300
gatctacatgt agcttggcag aactgactttt gtggactctg cggttatattt ctgtgcagat 360
ggtaaacgtat attactatgc tatggactac tgggttcaag gaaaccttcaatg caccgttctcc 420
tcagggtggag ggggttcaagg tggggggggcc tctgggggttg gggatgtcgtt aattttttttt 480
acccatgttca ctgtttttttt agttgtatgtt ctggggcaga gggccaccat ctatgtggagg 540
ggcagcaaaa gtgtcaatgtt atctgggttat agttatatgtt actggtaacca acagaaaacca 600

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ggacagccac ccaaactctt catctatctt gcatccaaac tagaatctgg ggtccctgtcc 660
aggttcagtgc cagtgccgttc tggacacat ttcacccctca acatccatcc tttggaggag 720
gaggatgctg caacccattttt ctgtcagcac agtagggagc ttccctggac ttccctggaa 780
ggccaccaaggc tggaaatcaa aacggccggcc tcagaacaaa aactcatctc agaaaggat 840
ctgaatgggg cggcacatca ccatcaccat cactaa 876

<311> 102

<311> 291

<311> PRT

<313> Artificial Sequence

<410>

<413> Description of the artificial sequence:scFv region

<400> 102

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
261 265 271

Gln Lys Ile Ile Ser Glu Glu Asp Ile Asn Gly Ala Ala His His His
 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345

His His His

<210> 103
<211> P4
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

4300 103
tgtccatgtaa caaaaactca tctcagaaga ggatctgaat gggggggcac atcaccatca 60
tcatcactaa taag 74

• 210• 104
• 211• 69
• 212• DNA
• 213• Artificial Sequence

(222) Description of the artificial sequence:primer

W100: 115
W110: 16
W120: PRT
n. 180: Artificial Sequence

4.200 4.201 Description of the artificial sequence:CDR3 region

44000 105
 Lys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
 1 5 10 15

4.10 - 136
4.11 - 16
4.12 - PRT
4.13 - Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

400-106
 Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp
 1 5 10 15